```
==========================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=7; day=27; hr=11; min=15; sec=3; ms=141; ]
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Reviewer Comments:
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          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1               5                      10


cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15              20              25                      30


agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35              40              45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50              55              60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65              70              75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291


Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80              85              90
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Please remove the blank line between the above row of codons and their
respective amino acids; the amino acids should appear directly below
their their codons.

<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 15
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            1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147

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Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
              35                  40                  45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct    195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
              50                  55                  60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat    243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
              65                  70                  75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga    291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
          80                  85                  90


tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct    339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
    95                  100                 105                 110


gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc    387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                  115                 120                 125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
              130                 135                 140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
              145                 150                 155


ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa    531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
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gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt    579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190


atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
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gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
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        210   215   220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225   230   235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240   245   250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255   260   265   270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                    275   280   285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
        290   295   300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305   310   315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser
        320   325   330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335   340   345   350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
                    355   360   365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370   375   380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385   390   395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400   405   410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415   420   425   430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
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ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450   455   460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
            465   470   475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480   485   490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495   500   505   510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg   1576
Asn Asp Gly Ser Val Ile
            515

1) Please remove the blank line between the above row of codons and
their amino acids; 2) the above <220>-<223> section describing "k" at

location 1578 is incorrect; the sequence only has 1576 nucleotides.
Same errors in Sequences 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39 and
41.

<210> 33
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 33
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

```
          15                    20                    25                    30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                    35                    40                    45


ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
              50                    55                    60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65                    70                    75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80                    85                    90


tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
     95                   100                   105                   110


gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                   115                   120                   125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                   130                   135                   140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
              145                   150                   155


ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
         160                   165                   170


gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                   180                   185                   190
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atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
            195                     200                     205


gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                     215                     220


gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                     230                     235


cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
            240                     245                     250


cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                     260                     265                     270


ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                    275                     280                     285


gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                     295                     300


aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                     310                     315


cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser
            320                     325                     330


gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                     340                     345                     350


aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag    1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
```

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
        370   375   380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385   390   395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
        400   405   410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415   420   425   430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                        435   440   445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
        450   455   460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465   470   475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480   485   490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495   500   505   510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg   1576
Asn Asp Gly Ser Val Ile
                    515

Two errors above: 1) the <220>-<223> section describing the "y" at
location 1008 is errored: "g" is at locadtion 1008; 2) the <220>-<223>
section describing the "k" at location 1578 is errored: there are only
1576 nucleotides above.

          *

Validated By CRFValidator v 1.0.3

Application No: 10569000   Version No: 2.0

Input Set:

Output Set:

Started:	2010-07-22 16:44:17.022
Finished:	2010-07-22 16:44:19.919
Elapsed:	0 hr(s) 0 min(s) 2 sec(s) 897 ms
Total Warnings:	0
Total Errors:	112
No. of SeqIDs Defined:	42
Actual SeqID Count:	42

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
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E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

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          Input Set:


          Output Set:



             Started:   2010-07-22 16:44:17.022
            Finished:   2010-07-22 16:44:19.919
             Elapsed:   0 hr(s) 0 min(s) 2 sec(s) 897 ms
      Total Warnings:   0
        Total Errors:   112
 No. of SeqIDs Defined:  42
   Actual SeqID Count:   42
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Error code   Error Description

                  This error has occured more than 20 times, will not be displayed

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aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga    1020

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tgtgttatta aaaactgcaa gataaaccat tctgtagttg gactccgatc ttgcatatct    1140

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gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc    1260

atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat    1320

gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt    1380

gtcacagtga tcaaggatgc tttactccct agtggaacag ttata                    1425


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<212>  PRT
<213>  zea mays

<400>  2

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Trp Asn Ala
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            20                  25                  30

Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65                  70                  75                  80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145                 150                 155                 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165                 170                 175
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
        180   185   190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195   200   205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
        210   215   220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225   230   235   240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245   250   255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
        260   265   270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
        275   280   285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
        290   295   300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305   310   315   320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
        325   330   335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
        340   345   350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
        355   360   365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370   375   380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385   390   395   400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
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Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
        420   425   430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
        435   440   445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
        450   455   460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465   470   475

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<212> DNA
<213> zea mays

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aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat ggagggtac   360

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caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa   600

cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct   660

gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt   720

gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc   780

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gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct gtatgatggt   900

tactgggaag atatcggtac cattgcggca tttttataatg caaacttggg aataaccaag   960

aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga   1020

cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggtgaagga   1080

tgtgttatta aaaactgcaa gataaaccat tctgtagttg gactccgatc ttgcatatct   1140

gaaggtgcta tcatagagga cagtttacta atgggtgcgg actactatga gacagaagct   1200

gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc   1260

atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat   1320

gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt   1380

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<212> PRT
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Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Trp Asn Ala
1   5   10   15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
                20   25   30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35   40   45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
        50   55   60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65   70   75   80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85   90   95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
                100   105   110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
            115   120   125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
            130   135   140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145   150   155   160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165   170   175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
                180   185   190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
            195   200   205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
            210   215   220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225   230   235   240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245   250   255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
            260   265   270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
            275   280   285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
        290   295   300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305   310   315   320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
            325   330   335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
            340   345   350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
            355   360   365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370   375   380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385   390   395   400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
            405   410   415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
            420   425   430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465   470   475

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<212>   DNA
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caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac   180

cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt   240

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tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac      420

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gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc      540

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aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct     1020

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aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaaggtgga     1380

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<212>    PRT
<213>    zea mays

<400>    6

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Trp Asn Ala
1                5                   10                  15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
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                35                    40                      45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50                    55                    60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                    70                    75                    80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                    90                    95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
                100                   105                  110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
                115                   120                  125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
                130                   135                  140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145                   150                   155                  160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
                165                   170                  175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
                180                   185                  190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
                195                   200                  205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210                   215                  220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225                   230                   235                  240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
                245                   250                  255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
                260                   265                  270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
                275                   280                  285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
290                   295                   300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305                   310                   315                  320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
                325                   330                  335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
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                340                      345                      350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
        355                      360                      365


Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370                      375                      380


Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                      390                      395                      400


Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
                405                      410                      415


Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
                420
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